NIST Conference on Microarray Standards

Validation of the Affymetrix Microarray System and the Challenges Faced

R D Hockett, MD Senior Clinical Research Physician Group Leader Genomic Medicine





NIST Standards Conference

- Brief Description of Clinical Trial
- Validation plan for the Affymetrix Array
 - Defining Variability
 - Establishing Control Ranges
 - Testing controls

Investigating Parameters around RNA Quality



Study Objectives

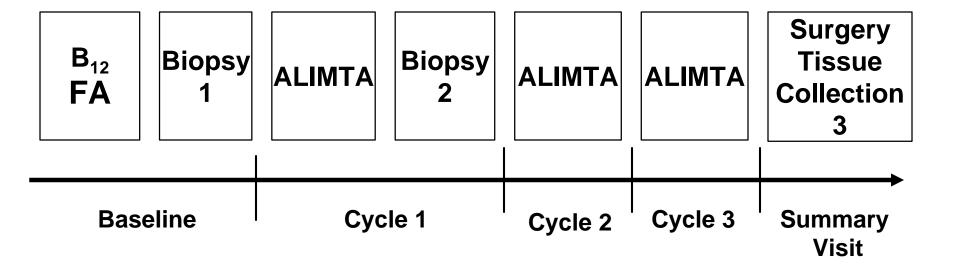
- Correlation of tumor tissue derived biomarkers and clinical outcome at:
 - Baseline (prior to treatment)
 - 24 hrs after first dose of ALIMTA
 - After 3 cycles of ALIMTA

• Clinical response and standard efficacy and safety end-points

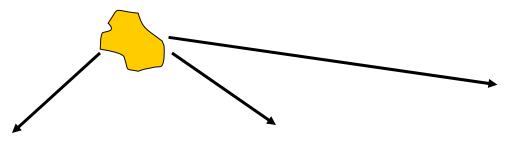


Study Design

Hcys MMA Other Labs



Distribution of Tissues



Histology,

Immunohistochemistry,

and/or FISH

•H & E

•TS

•DHFR

•GARFT

•p53

•erbB-2

Quantitative PCR

•TS

•DHFR

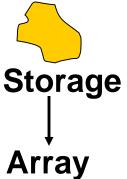
GARFT

•p53

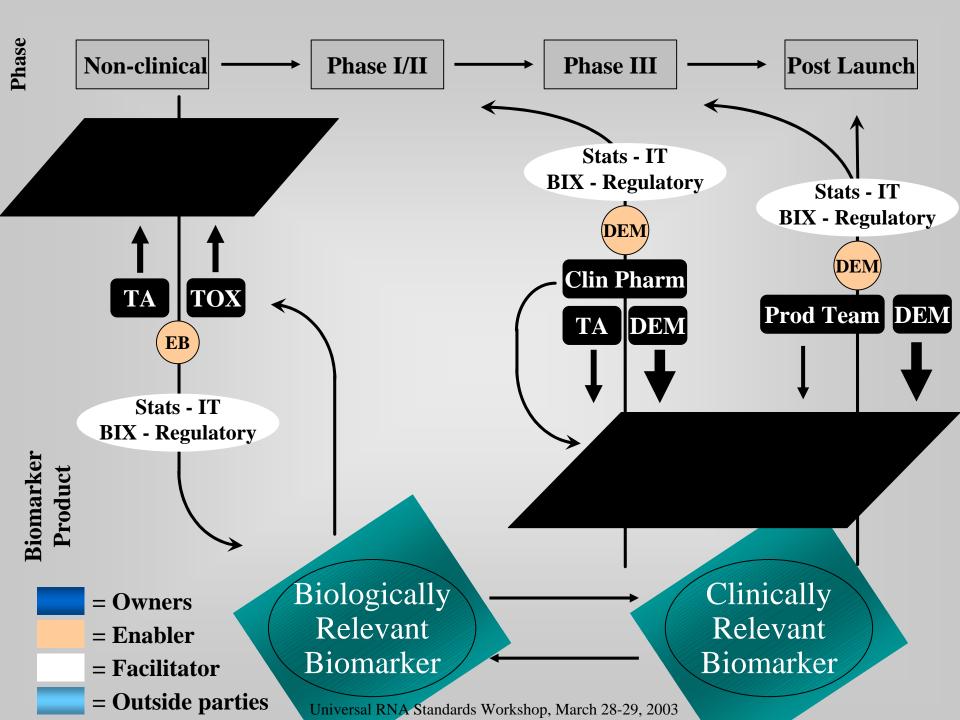
•erbB-2

•b-actin

•others



Profiling



Clinical Validation of Microarrays

- Validation Process
 - Establish Instrument Parameters
 - Comply with CFR 21 part 11
 - Define Variability
 - Accuracy
 - Precision
 - Set Standards
 - Establish Control Parameters
 - Acceptance/Rejection Criteria
 - Validation Document



Clinical Validation of Microarrays

Orders of magnitude increase in the number of analytes

Example:
Detector Calibrators

Example:
Standard curves
Control Performance
Metrics

Instrument controls to check electronics/detection

Proficiency Testing

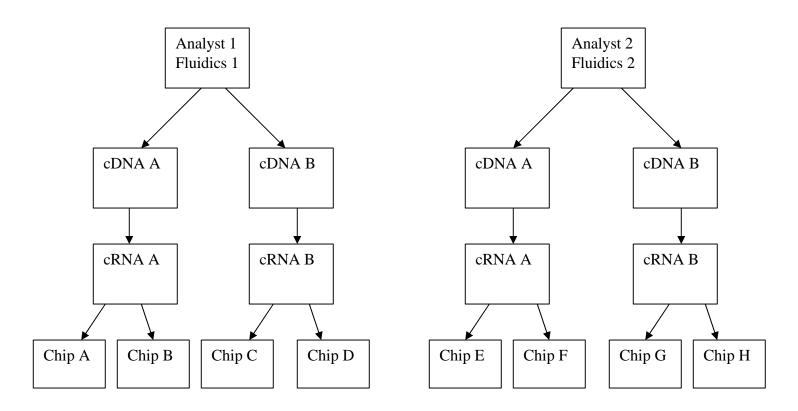
Individual standards and controls for each assay

- Experiment #1 Define procedure variability
 - How many times should each step be run for a valid result?
 - How many extractions?
 - cDNA syntheses?
 - cRNA labelings?
 - Chips?
 - Define variability of each step, including technologist and fluidics workstations



- 7 runs will be completed by each technologist
 - For each run the analysts will be working side by side on the same day.
 - Each analyst will use 4 chips
 - Two lots of chips will be used
 - 4 runs one lot 3 runs second lot
- The fluidics stations will be alternated between analysts each run.
- The design for experiment 2 will be finalized using the results from experiment 1



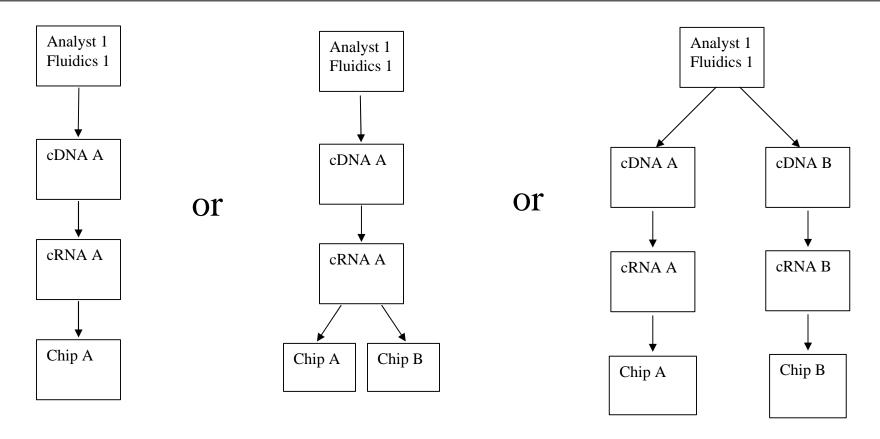


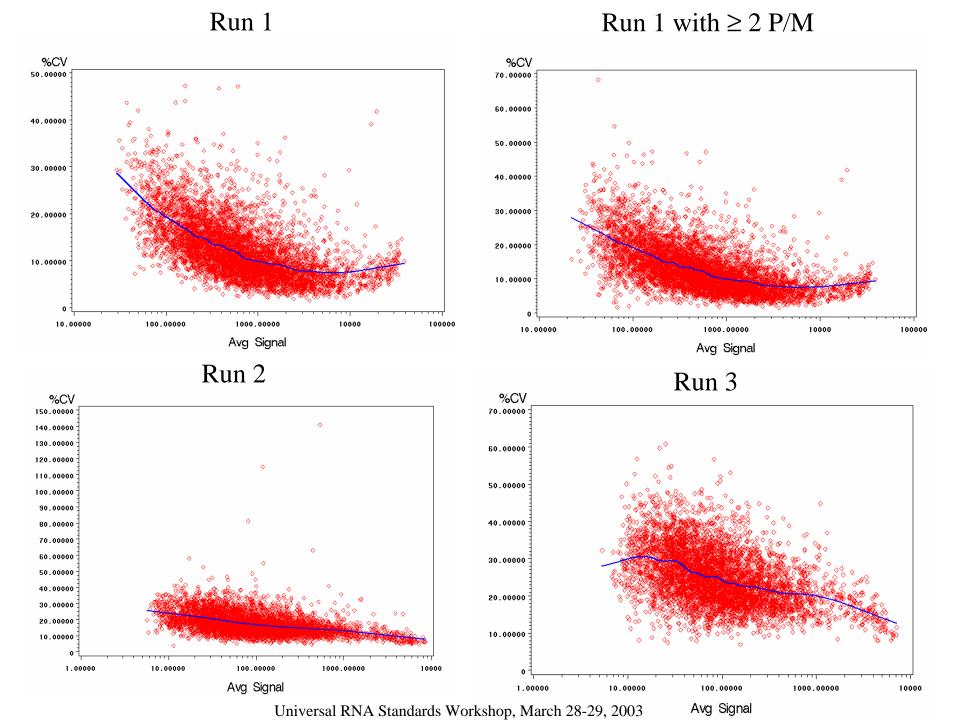
56 Chips Total
Data will determine subsequent procedure
24 Chips planned from tissue source



- Experiment #2 Establish control parameters
 - During clinical use, one of every 8 chips will be control
 - All genes checked for acceptance/rejection criteria
 - 2/3 of genes must be within acceptable limits or entire run of 8 chips must be repeated
 - Limits set by running control 25 30 times over different days by different analysts
 - Procedure set by experiment #1

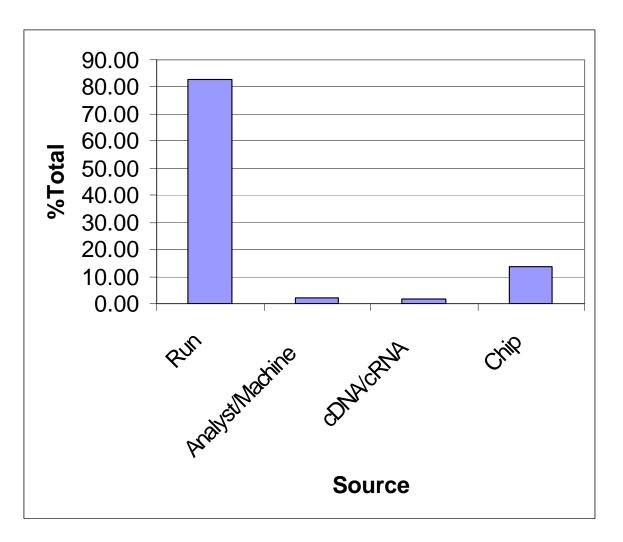






Average %Variance Explained Across Genes

	%Total
Effect	Variance
Run	82.74
Analyst/Machine	1.96
cDNA/cRNA	1.80
Chip	13.50



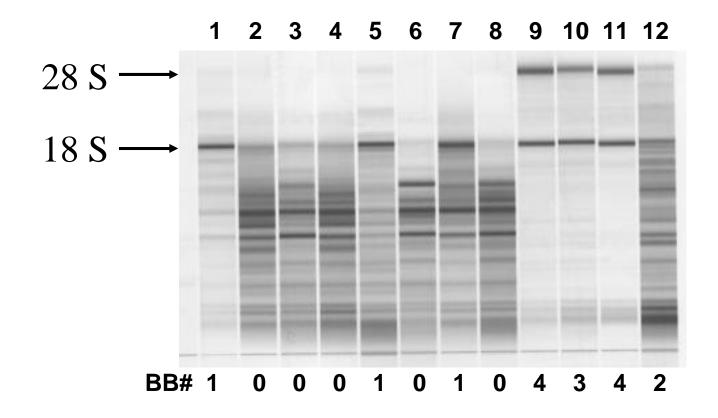


Sample Usefulness

- When collecting clinical samples, how much RNA degradation can be present and still get meaningful results?
 - Pristine?
 - Both 28S and 18S present?

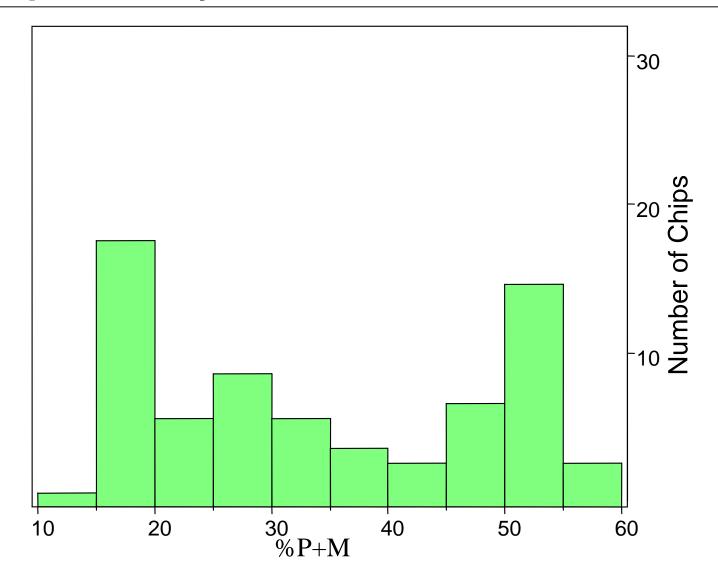


Sample Quality





Sample Quality





Sample Quality

Group	Sample ID	%P+M*	BB#	Group	Sample ID	%P+M*	BB#
1	LES-101	56.24	4	3	LES-39	54.13	3
1	LES-123	53.78	2	3	LES-98	53.61	4
1	LES-105	53.35	1	3	LES-34	52.56	3
1	LES-106	51.89	3	3	LES-33	51.60	4
1	LES-100	49.50	3	NA	LES-46	51.57	4
1	LES-96	47.83	2	3	LES-63	45.46	1
1	LES-153	36.62	1	3	LES-103	45.28	1
1	LES-131	33.78	1	NA	LES-43	44.60	2
1	LES-3	32.74	2	2	LES-61	33.57	1
1	LES-57	29.11	1	3	LES-134	31.74	2
1	LES-45	29.09	0	3	LES-86	22.96	1
1	LES-50	26.52	1	3	L3S-5	21.08	1
1	LES-155	25.84	1	3	LES-7	19.87	0
1	LES-62	25.51	1	3	LES-92	19.02	1
1	LES-22	19.63	1	2	LES-64	18.82	1
1	LES-27	17.55	0	3	LES-90	17.89	1
1	LES-88	17.31	0	2	LES-6	17.74	0
1	LES-59	15.48	1	2	LES-4	14.94	1

BB#	Proportion "Useful"	% Usable
0	0/5	0
1	4/18	22%
2	3/5	60%
3	4/4	100%
4	4/4	100%

$$r = 0.78$$

 $p = 1.90E-08$



^{*}Average of two chips.